04CO 03-08-01
#2 OIPE

RAW SEQUENCE LISTING DATE: 03/02/2001
PATENT APPLICATION: US/09/776,865 TIME: 13:48:32

Input Set : A:\Sequence.txt
Output Set: N:\CRF3\03022001\I776865.raw

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  3 <110> APPLICANT: Hellerqvist, Carl
  5 <120> TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
  7 <130> FILE REFERENCE: 22100-0100 46126-252687
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/776,865
C--> 9 <141> CURRENT FILING DATE: 2001-02-02
  9 <150> PRIOR APPLICATION NUMBER: US 60/179,870
 10 <151> PRIOR FILING DATE: 2000-02-02
 12 <160> NUMBER OF SEQ ID NOS: 4
 14 <170> SOFTWARE: PatentIn version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2930
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (263)..(1870)
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 30 gcgggagacg gtcgtccgaa caccggctcc ccggcatgcg tagaccggcg ggcggagcgg    180
 32 gctcactttg cgccaatcct acgagaactc ccagaactcc gcttccctag tccaacccaa    240
 34 gccagagttg cccacaccta ag atg gcg gcg ggg gcg atg aca ccg ccc cgc     292
 35                         Met Ala Ala Gly Ala Met Thr Pro Pro Arg
 36                         1               5                  10
 38 ccg gtc cag cca gct cgg ccc ggg ggc ttc ggg ctg tcg ggc cgg cgc      340
 39 Pro Val Gln Pro Ala Arg Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg
 40                 15                  20                  25
 42 tcc ctt ctc tgc cag gtg gcg agt aca cct gct cac gta ggc gtc atg      388
 43 Ser Leu Leu Cys Gln Val Ala Ser Thr Pro Ala His Val Gly Val Met
 44             30                  35                  40
 46 agg tct ccg gtt cga gac ctg gcc cgg aac gat ggc gag gag agc acg      436
 47 Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser Thr
 48         45                  50                  55
 50 gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct cca      484
 51 Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro
 52     60                  65                  70
 54 gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt ggt      532
 55 Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly
 56 75                  80                  85                  90
 58 ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta gtg      580
 59 Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu Val
 60                 95                  100                 105
 62 gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc aag      628
 63 Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys
 64             110                 115                 120
 66 gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa acg      676
 67 Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln Thr
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68          125                 130                 135
70 ggt aag aag tac caa tgg gat gca gaa act caa gga tgg att ctc ggt      724
71 Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly
72      140                 145                 150
74 tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat gtt      772
75 Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val
76 155                 160                 165                 170
78 gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt ggc      820
79 Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu Gly
80                  175                 180                 185
82 act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga gtt      868
83 Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly Val
84              190                 195                 200
86 gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt gtt      916
87 Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly Val
88          205                 210                 215
90 aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct ctt      964
91 Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro Leu
92      220                 225                 230
94 gaa aga agc aaa ctt ctt agc att tcg tat gca gga gca cag ctt ggg     1012
95 Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly
96 235                 240                 245                 250
98 aca gta att tct ctt cct ctt tct gga ata att tgc tac tat atg aat     1060
99 Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn
100                 255                 260                 265
102 tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg ttt     1108
103 Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe
104             270                 275                 280
106 ctt ttg tgg atc tgg tta gtt agt gac aca cca caa aaa cac aag aga     1156
107 Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys Arg
108         285                 290                 295
110 att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat cag     1204
111 Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln
112     300                 305                 310
114 ctt tct tca cag aag tca gtg ccg tgg gta ccc att tta aaa tcc ctg     1252
115 Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser Leu
116 315                 320                 325                 330
118 cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act ttt     1300
119 Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr Phe
120                 335                 340                 345
122 tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta agg     1348
123 Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg
124             350                 355                 360
126 ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta ggc     1396
127 Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly
128         365                 370                 375
130 tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta agg     1444
131 Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg
132     380                 385                 390
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134 gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc ctt     1492
135 Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser Leu
136 395                 400                 405                 410
138 ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc att     1540
139 Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe Ile
140                 415                 420                 425
142 ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca aca     1588
143 Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr Thr
144             430                 435                 440
146 ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat att     1636
147 Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp Ile
148         445                 450                 455
150 gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt gcc     1684
151 Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala
152     460                 465                 470
154 act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc cct     1732
155 Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr Pro
156 475                 480                 485                 490
158 gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct gct     1780
159 Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala
160                 495                 500                 505
162 att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt gaa     1828
163 Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu
164             510                 515                 520
166 gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac             1870
167 Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
168         525                 530                 535
170 tgaaggaacc aataaataat cctgcctcta ttaatgtatt tttatttatc atgtaacctc   1930
172 aaagtgcctt ctgtattgtg taagcattct atgtcttttt ttaattgtac ttgtattaga   1990
174 tttttaaggc ctataatcat gaaatatcac tagttgccag aataataaaa tgaactgtgt   2050
176 ttaattatga ataatatgta agctaggact tctactttag gttcacatac ctgcctgcta   2110
178 gtcgggcaac atgaagtagg acagttctgt tgatttttta gggccatact aaagggaatg   2170
180 agctgaaaca gacctcctga taccttttgct taattaaact agatgataat tctcaggtac   2230
182 tgataaacac ctgttgttgt tcactttcct cataaaaatt gtcagctctc tctgacactt   2290
184 agacctcaaa ctttagcatc tctgtggagc tgccatccac tgtataattt cgcctggcaa   2350
186 ctggactgag gggagtgtgc ccaggcagct gccaagcact ccctccctgg cttcagggtc   2410
188 agagtgccca gcgtttatca gaggcagcat ccaagcccag agccagtgtc gactcttcgg   2470
190 ctggtgcctt tcctctgagg ggctatcaat gtgtagataa agccctgagt aggcaagagc   2530
192 agtgagatcc actgctatgg tcttgataca tcctcaaact ttcccttccc agcacagagg   2590
194 aatattggct ggcatgcaac ctgcaaaaga aaaatgcgaa gcggccgggc acggtggctc   2650
196 atgcctgtaa tcccagcact ttgggggget gaggtgggcg aatcatgaga tcaggagttc   2710
198 gagaccagcc tggccagcat ggtgaaaccc catctctact aaaaatacaa aaaattagct   2770
200 gggcgtggtg acgggcgcct gtaatcccag atactcagga ggctgaggta ggagaatcac   2830
202 ttgaacctgg gaggtggaag ttgcagtgaa ccaagatcac gccactgcac tccagcctgg   2890
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207 <210> SEQ ID NO: 2
208 <211> LENGTH: 536
209 <212> TYPE: PRT
210 <213> ORGANISM: Homo sapiens
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212 <400> SEQUENCE: 2
214 Met Ala Ala Gly Ala Met Thr Pro Pro Arg Pro Val Gln Pro Ala Arg
215 1 5 10 15
218 Pro Gly Gly Phe Gly Leu Ser Gly Arg Arg Ser Leu Leu Cys Gln Val
219 20 25 30
222 Ala Ser Thr Pro Ala His Val Gly Val Met Arg Ser Pro Val Arg Asp
223 35 40 45
226 Leu Ala Arg Asn Asp Gly Glu Ser Thr Asp Arg Thr Pro Leu Leu
227 50 55 60
230 Pro Gly Ala Pro Arg Ala Glu Ala Ala Pro Val Cys Cys Ser Ala Arg
231 65 70 75 80
234 Tyr Asn Leu Ala Ile Leu Ala Phe Phe Gly Phe Phe Ile Val Tyr Ala
235 85 90 95
238 Leu Arg Val Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn
239 100 105 110
242 Thr Thr Leu Glu Asp Asn Arg Thr Ser Lys Ala Cys Pro Glu His Ser
243 115 120 125
246 Ala Pro Ile Lys Val His His Asn Gln Thr Gly Lys Lys Tyr Gln Trp
247 130 135 140
250 Asp Ala Glu Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr
251 145 150 155 160
254 Ile Ile Thr Gln Ile Pro Gly Gly Tyr Val Ala Ser Lys Ile Gly Gly
255 165 170 175
258 Lys Met Leu Leu Gly Phe Gly Ile Leu Gly Thr Ala Val Leu Thr Leu
259 180 185 190
262 Phe Thr Pro Ile Ala Ala Asp Leu Gly Val Gly Pro Leu Ile Val Leu
263 195 200 205
266 Arg Ala Leu Glu Gly Leu Gly Glu Gly Val Thr Phe Pro Ala Met His
267 210 215 220
270 Ala Met Trp Ser Ser Trp Ala Pro Pro Leu Glu Arg Ser Lys Leu Leu
271 225 230 235 240
274 Ser Ile Ser Tyr Ala Gly Ala Gln Leu Gly Thr Val Ile Ser Leu Pro
275 245 250 255
278 Leu Ser Gly Ile Ile Cys Tyr Tyr Met Asn Trp Thr Tyr Val Phe Tyr
279 260 265 270
282 Phe Phe Gly Thr Ile Gly Ile Phe Trp Phe Leu Leu Trp Ile Trp Leu
283 275 280 285
286 Val Ser Asp Thr Pro Gln Lys His Lys Arg Ile Ser His Tyr Glu Lys
287 290 295 300
290 Glu Tyr Ile Leu Ser Ser Leu Arg Asn Gln Leu Ser Ser Gln Lys Ser
291 305 310 315 320
294 Val Pro Trp Val Pro Ile Leu Lys Ser Leu Pro Leu Trp Ala Ile Val
295 325 330 335
298 Val Ala His Phe Ser Tyr Asn Trp Thr Phe Tyr Thr Leu Leu Thr Leu
299 340 345 350
302 Leu Pro Thr Tyr Met Lys Glu Ile Leu Arg Phe Asn Val Gln Glu Asn
303 355 360 365
306 Gly Phe Leu Ser Ser Leu Pro Tyr Leu Gly Ser Trp Leu Cys Met Ile
307 370 375 380

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310 Leu Ser Gly Gln Ala Ala Asp Asn Leu Arg Ala Lys Trp Asn Phe Ser
311 385                 390                 395                 400
314 Thr Leu Cys Val Arg Arg Ile Phe Ser Leu Ile Gly Met Ile Gly Pro
315                 405                 410                 415
318 Ala Val Phe Leu Val Ala Ala Gly Phe Ile Gly Cys Asp Tyr Ser Leu
319             420                 425                 430
322 Ala Val Ala Phe Leu Thr Ile Ser Thr Thr Leu Gly Gly Phe Cys Ser
323         435                 440                 445
326 Ser Gly Phe Ser Ile Asn His Leu Asp Ile Ala Pro Ser Tyr Ala Gly
327     450                 455                 460
330 Ile Leu Leu Gly Ile Thr Asn Thr Phe Ala Thr Ile Pro Gly Met Val
331 465                 470                 475                 480
334 Gly Pro Val Ile Ala Lys Ser Leu Thr Pro Asp Asn Thr Val Gly Glu
335                 485                 490                 495
338 Trp Gln Thr Val Phe Tyr Ile Ala Ala Ala Ile Asn Val Phe Gly Ala
339             500                 505                 510
342 Ile Phe Phe Thr Leu Phe Ala Lys Gly Glu Val Gln Asn Trp Ala Leu
343         515                 520                 525
346 Asn Asp His His Gly His Arg His
347     530                 535
350 <210> SEQ ID NO: 3
351 <211> LENGTH: 2844
352 <212> TYPE: DNA
353 <213> ORGANISM: Ovis sp.
355 <220> FEATURE:
356 <221> NAME/KEY: CDS
357 <222> LOCATION: (84)..(1568)
359 <400> SEQUENCE: 3
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362 cgccgtagct ccctgaaggc atc atg aag tcc ccg gtt tcg gac tta gcc ccg    113
363                           Met Lys Ser Pro Val Ser Asp Leu Ala Pro
364                           1               5                   10
366 agc gac ggc gag gag ggc tcg gac cgc aca ccg ctc ctg cag cgc gcc     161
367 Ser Asp Gly Glu Glu Gly Ser Asp Arg Thr Pro Leu Leu Gln Arg Ala
368                 15                  20                  25
370 ccg cgg gcg gaa ccc gct cca gta tgc tgc tct gct cgt tac aac cta     209
371 Pro Arg Ala Glu Pro Ala Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu
372             30                  35                  40
374 gca ttt ttg tcc ttt ttt ggt ttc ttc gtt ctc tat tca tta cgg gtg     257
375 Ala Phe Leu Ser Phe Phe Gly Phe Phe Val Leu Tyr Ser Leu Arg Val
376         45                  50                  55
378 aat ctg agc gtt gca cta gtg gac atg gtg gat tca aac aca act gcc     305
379 Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn Thr Thr Ala
380     60                  65                  70
382 aaa gat aat aga acg tcc tac gag tgt gca gag cat tct gct ccc ata     353
383 Lys Asp Asn Arg Thr Ser Tyr Glu Cys Ala Glu His Ser Ala Pro Ile
384 75                  80                  85                  90
386 aaa gtt ctt cac aac caa acg ggt aaa aag tac cgg tgg gat gca gaa     401
387 Lys Val Leu His Asn Gln Thr Gly Lys Lys Tyr Arg Trp Asp Ala Glu
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date